

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/515,806

DATE: 10/04/2000
TIME: 22:32:05

Input Set : A:\38155002.app
Output Set: N:\CRF3\10042000\I515806.raw

RECEIVED

OCT 17 2000

TECH CENTER 1600/2900

```

69 agg ctg ttg gag gcc aag cgg aaa gaa gag cag gag caa cgt gaa atc 587
70 Arg Leu Leu Glu Ala Lys Arg Lys Glu Glu Gln Glu Gln Arg Glu Ile
71 160 165 170 175
73 ctg cat gag att cag aga agg aaa gaa gag ata aaa gaa gag aaa aaa 635
74 Leu His Glu Ile Gln Arg Arg Lys Glu Glu Ile Lys Glu Glu Lys Lys
75 180 185 190
77 agg aaa gaa atg gct aag cag gaa cgt ttg gaa att gct agt ttg tca 683
78 Arg Lys Glu Met Ala Lys Gln Glu Arg Leu Glu Ile Ala Ser Leu Ser
79 195 200 205
81 aac caa gat cat acc tct aag aag gac cca gga gga cac aga acg gct 731
82 Asn Gln Asp His Thr Ser Lys Lys Asp Pro Gly Gly His Arg Thr Ala
83 210 215 220
85 gcc att cta cat gga ggc tct cct gac ttt gta gga aat ggt aaa cat 779
86 Ala Ile Leu His Gly Gly Ser Pro Asp Phe Val Gly Asn Gly Lys His
87 225 230 235
89 cgg gca aac tcc tca gga agg tct agg cga gaa cgt cag tat tct gta 827
90 Arg Ala Asn Ser Ser Gly Arg Ser Arg Arg Glu Arg Gln Tyr Ser Val
91 240 245 250 255
93 tgt aat agt gaa gat tct cct ggc tct tgt gaa att ctg tat ttc aat 875
94 Cys Asn Ser Glu Asp Ser Pro Gly Ser Cys Glu Ile Leu Tyr Phe Asn
95 260 265 270
97 atg ggg agt cct gat cag ctg atg gtg cac aaa ggg aaa tgt att ggc 923
98 Met Gly Ser Pro Asp Gln Leu Met Val His Lys Gly Lys Cys Ile Gly
99 275 280 285
101 agt gat gaa caa ctt gga aaa tta gtc tac aat gct ttg gaa aca gcc 971
102 Ser Asp Glu Gln Leu Gly Lys Leu Val Tyr Asn Ala Leu Glu Thr Ala
103 290 295 300
105 act ggt ggc ttt gtc ttg ttg tat gag tgg gtc ctt cag tgg cag aaa 1019
106 Thr Gly Gly Phe Val Leu Leu Tyr Glu Trp Val Leu Gln Trp Gln Lys
107 305 310 315
109 aaa atg ggt cca ttc ctt acc agt caa gaa aaa gag aag att gat aag 1067
110 Lys Met Gly Pro Phe Leu Thr Ser Gln Glu Lys Glu Lys Ile Asp Lys
111 320 325 330 335
113 tgc aaa aag cag att caa gga aca gaa aca gaa ttc aac tca ctg gta 1115
114 Cys Lys Lys Gln Ile Gln Gly Thr Glu Thr Glu Phe Asn Ser Leu Val
115 340 345 350
117 aaa ttg agc cat cca aat gta gta cgc tac ctt gca atg aat ctg aaa 1163
118 Lys Leu Ser His Pro Asn Val Val Arg Tyr Leu Ala Met Asn Leu Lys
119 355 360 365
121 gag caa gac gac tcc atc gtg gtg gac att tta gtg gag cac att agt 1211
122 Glu Gln Asp Asp Ser Ile Val Val Asp Ile Leu Val Glu His Ile Ser
123 370 375 380
125 ggg gtc tct ctt gct gca cac ctg agc cac tca ggc ccc atc cct gtg 1259
126 Gly Val Ser Leu Ala Ala His Leu Ser His Ser Gly Pro Ile Pro Val
127 385 390 395
129 cat cag ctt cgc agg tac aca gct cag ctg ctg tca ggc ctt gat tat 1307
130 His Gln Leu Arg Arg Tyr Thr Ala Gln Leu Leu Ser Gly Leu Asp Tyr
131 400 405 410 415
133 ctg cac agc aat tct gtg gtg cat aag gtc ctg agt gca tct aat gtc 1355

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134 Leu His Ser Asn Ser Val Val His Lys Val Leu Ser Ala Ser Asn Val
135          420          425          430
137 ttg gtg gat gca gaa ggc acc gtc aag att acg gac tat agc att tct 1403
138 Leu Val Asp Ala Glu Gly Thr Val Lys Ile Thr Asp Tyr Ser Ile Ser
139          435          440          445
141 aag cgc ctc gca gac att tgc aag gag gat gtg ttt gag caa acc cga 1451
142 Lys Arg Leu Ala Asp Ile Cys Lys Glu Asp Val Phe Glu Gln Thr Arg
143          450          455          460
145 gtt cgt ttt agt gac aat gct ctg cct tat aaa acg ggg aag aaa gga 1499
146 Val Arg Phe Ser Asp Asn Ala Leu Pro Tyr Lys Thr Gly Lys Lys Gly
147          465          470          475
149 gat gtt tgg cgt ctt ggc ctt ctg ctg ctg tcc ctc agc caa gga cag 1547
150 Asp Val Trp Arg Leu Glu Leu Leu Leu Ser Leu Ser Gln Gly Gln
151 480          485          490          495
153 gaa tgt gga gag tac cct gtg acc atc cct agt gac tta cca gct gac 1595
154 Glu Cys Gly Glu Tyr Pro Val Thr Ile Pro Ser Asp Leu Pro Ala Asp
155          500          505          510
157 ttt caa gat ttt cta aag aaa tgt gtg tgc ttg gat gac aag gaa aga 1643
158 Phe Gln Asp Phe Leu Lys Lys Cys Val Cys Leu Asp Asp Lys Glu Arg
159          515          520          525
161 tgg agt ccc cag cag ttg ttg aaa cac agc ttt ata aat ccc cag cca 1691
162 Trp Ser Pro Gln Gln Leu Leu Lys His Ser Phe Ile Asn Pro Gln Pro
163          530          535          540
165 aaa atg cct cta gtg gaa caa agt cct gaa gat tct gga gga caa gat 1739
166 Lys Met Pro Leu Val Glu Gln Ser Pro Glu Asp Ser Gly Gly Gln Asp
167          545          550          555
169 tat gtt gag act gtt att cct agc aac cgg cta ccc agt gct gcc ttc 1787
170 Tyr Val Glu Thr Val Ile Pro Ser Asn Arg Leu Pro Ser Ala Ala Phe
171 560          565          570          575
173 ttt agt gag aca cag aga cag ttt tcc cga tac ttc att gag ttt gaa 1835
174 Phe Ser Glu Thr Gln Arg Gln Phe Ser Arg Tyr Phe Ile Glu Phe Glu
175          580          585          590
177 gaa tta caa ctt ctt ggt aaa gga gct ttt gga gct gtc atc aag gtg 1883
178 Glu Leu Gln Leu Leu Gly Lys Gly Ala Phe Gly Ala Val Ile Lys Val
179          595          600          605
181 cag aac aag ttg gac ggc tgc tgc tac gca gtg aag cgc atc ccc atc 1931
182 Gln Asn Lys Leu Asp Gly Cys Cys Tyr Ala Val Lys Arg Ile Pro Ile
183          610          615          620
185 aac ccg gcc agc cgg cag ttc cgc agg atc aag ggc gaa gtg aca ctg 1979
186 Asn Pro Ala Ser Arg Gln Phe Arg Arg Ile Lys Gly Glu Val Thr Leu
187          625          630          635
189 ctg tca cgg ctg cac cat gag aac att gtg cgc tac tac aac gcc tgg 2027
190 Leu Ser Arg Leu His His Glu Asn Ile Val Arg Tyr Tyr Asn Ala Trp
191 640          645          650          655
193 atc gag cgg cac gag cgg ccg gcg gga ccg ggg acg ccg ccc ccg gac 2075
194 Ile Glu Arg His Glu Arg Pro Ala Gly Pro Gly Thr Pro Pro Asp
195          660          665          670
197 tcc ggg ccc ctg gcc aag gat gac cga gct gca cgc ggg cag ccg gcg 2123
198 Ser Gly Pro Leu Ala Lys Asp Asp Arg Ala Ala Arg Gly Gln Pro Ala

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199          675          680          685
201 agc gac aca gac ggc ctg gac agc gta gag gcc gcc gcg ccg cca ccc 2171
202 Ser Asp Thr Asp Gly Leu Asp Ser Val Glu Ala Ala Pro Pro Pro
203          690          695          700
205 atc ctc agc agc tcg gtg gag tgg agc act tcg gcc gag cgc tcg gcc 2219
206 Ile Leu Ser Ser Ser Val Glu Trp Ser Thr Ser Gly Glu Arg Ser Ala
207          705          710          715
209 agt gcc cgt ttc ccc gcc acc ggc ccg gcc tcc agc gat gac gag gac 2267
210 Ser Ala Arg Phe Pro Ala Thr Gly Pro Gly Ser Ser Asp Asp Glu Asp
211 720          725          730          735
213 gac gac gag gac gag cac ggt gcc gtc ttc tcc cag tcc ttc ctg cct 2315
214 Asp Asp Glu Asp Glu His Gly Gly Val Phe Ser Gln Ser Phe Leu Pro
215          740          745          750
217 gct tca gat tct gaa agt gat att atc ttt gac aat gaa gat gag aac 2363
218 Ala Ser Asp Ser Glu Ser Asp Ile Ile Phe Asp Asn Glu Asp Glu Asn
219          755          760          765
221 agt aaa agt cag aat cag gat gaa gat tgc aat gaa aag aat gcc tgc 2411
222 Ser Lys Ser Gln Asn Gln Asp Glu Asp Cys Asn Glu Lys Asn Gly Cys
223          770          775          780
225 cat gaa agt gag cca tca gtg acg act gag gct gtg cac tac cta tac 2459
226 His Glu Ser Glu Pro Ser Val Thr Thr Glu Ala Val His Tyr Leu Tyr
227          785          790          795
229 atc cag atg gag tac tgt gag aag agc act tta cga gac acc att gac 2507
230 Ile Gln Met Glu Tyr Cys Glu Lys Ser Thr Leu Arg Asp Thr Ile Asp
231 800          805          810          815
233 cag gga ctg tat cga gac acc gtc aga ctc tgg agg ctt ttt cga gag 2555
234 Gln Gly Leu Tyr Arg Asp Thr Val Arg Leu Trp Arg Leu Phe Arg Glu
235          820          825          830
237 att ctg gat gga tta gct tat atc cat gag aaa gga atg att cac cgg 2603
238 Ile Leu Asp Gly Leu Ala Tyr Ile His Glu Lys Gly Met Ile His Arg
239          835          840          845
241 gat ttg aag cct gtc aac att ttt ttg gat tct gat gac cat gtg aaa 2651
242 Asp Leu Lys Pro Val Asn Ile Phe Leu Asp Ser Asp Asp His Val Lys
243          850          855          860
245 ata ggt gat ttt ggt ttg gcg aca gac cat cta gcc ttt tct gct gac 2699
246 Ile Gly Asp Phe Gly Leu Ala Thr Asp His Leu Ala Phe Ser Ala Asp
247          865          870          875
249 agc aaa caa gac gat cag aca gga gac ttg att aag tca gac cct tca 2747
250 Ser Lys Gln Asp Asp Gln Thr Gly Asp Leu Ile Lys Ser Asp Pro Ser
251 880          885          890          895
253 ggt cac tta act ggg atg gtt gcc act gct ctc tat gta agc cca gag 2795
254 Gly His Leu Thr Gly Met Val Gly Thr Ala Leu Tyr Val Ser Pro Glu
255          900          905          910
257 gtc caa gga agc acc aaa tct gca tac aac cag aaa gtg gat ctc ttc 2843
258 Val Gln Gly Ser Thr Lys Ser Ala Tyr Asn Gln Lys Val Asp Leu Phe
259          915          920          925
261 agc ctg gga att atc ttc ttt gag atg tcc tat cac ccc atg gtc acg 2891
262 Ser Leu Gly Ile Ile Phe Phe Glu Met Ser Tyr His Pro Met Val Thr
263          930          935          940

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```

265 gct tca gaa agg atc ttt gtt ctc aac caa ctc aga gat ccc act tcg 2939
266 Ala Ser Glu Arg Ile Phe Val Leu Asn Gln Leu Arg Asp Pro Thr Ser
267 945 950 955
269 cct aag ttt cca gaa gac ttt gac gat gga gag cat gca aag cag aaa 2987
270 Pro Lys Phe Pro Glu Asp Phe Asp Asp Gly Glu His Ala Lys Gln Lys
271 960 965 970 975
273 tca gtc atc tcc tgg ctg ttg aac cac gat cca gca aaa cgg ccc aca 3035
274 Ser Val Ile Ser Trp Leu Leu Asn His Asp Pro Ala Lys Arg Pro Thr
275 980 985 990
277 gcc aca gaa ctg ctc aag agt gag ctg ctc ccc cca ccc cag atg gag 3083
278 Ala Thr Glu Leu Leu Lys Ser Glu Leu Leu Pro Pro Pro Gln Met Glu
279 995 1000 1005
281 gag tca gag ctg cat gaa gtg ctg cac cac acg ctg acc aac gtg gat 3131
282 Glu Ser Glu Leu His Glu Val Leu His His Thr Leu Thr Asn Val Asp
283 1010 1015 1020
285 ggg aag gcc tac cgc acc atg atg gcc cag atc ttc tcg cag cgc atc 3179
286 Gly Lys Ala Tyr Arg Thr Met Met Ala Gln Ile Phe Ser Gln Arg Ile
287 1025 1030 1035
289 tcc cct gcc atc gat tac acc tat gac agc gac ata ctg aag ggc aac 3227
290 Ser Pro Ala Ile Asp Tyr Thr Tyr Asp Ser Asp Ile Leu Lys Gly Asn
291 1040 1045 1050 1055
293 ttc tca atc cgt aca gcc aag atg cag cag cat gtg tgt gaa acc atc 3275
294 Phe Ser Ile Arg Thr Ala Lys Met Gln Gln His Val Cys Glu Thr Ile
295 1060 1065 1070
297 atc cgc atc ttt aaa aga cat gga gct gtt cag ttg tgt act cca cta 3323
298 Ile Arg Ile Phe Lys Arg His Gly Ala Val Gln Leu Cys Thr Pro Leu
299 1075 1080 1085
301 ctg ctt ccc cga aac aga caa ata tat gag cac aac gaa gct gcc cta 3371
302 Leu Leu Pro Arg Asn Arg Gln Ile Tyr Glu His Asn Glu Ala Ala Leu
303 1090 1095 1100
305 ttc atg gac cac agc ggg atg ctg gtg atg ctt cct ttt gac ctg cgg 3419
306 Phe Met Asp His Ser Gly Met Leu Val Met Leu Pro Phe Asp Leu Arg
307 1105 1110 1115
309 atc cct ttt gca aga tat gtg gca aga aat aat ata ttg aat tta aaa 3467
310 Ile Pro Phe Ala Arg Tyr Val Ala Arg Asn Asn Ile Leu Asn Leu Lys
311 1120 1125 1130 1135
313 cga tac tgc ata gaa cgt gtg ttc agg ccg cgc aag tta gat cga ttt 3515
314 Arg Tyr Cys Ile Glu Arg Val Phe Arg Pro Arg Lys Leu Asp Arg Phe
315 1140 1145 1150
317 cat ccc aaa gaa ctt ctg gag tgt gca ttt gat att gtc act tct acc 3563
318 His Pro Lys Glu Leu Leu Glu Cys Ala Phe Asp Ile Val Thr Ser Thr
319 1155 1160 1165
321 acc aac agc ttt ctg ccc act gct gaa att atc tac act atc tat gaa 3611
322 Thr Asn Ser Phe Leu Pro Thr Ala Glu Ile Ile Tyr Thr Ile Tyr Glu
323 1170 1175 1180
325 atc atc caa gag ttt cca gca ctt cag gaa aga aat tac agt att tat 3659
326 Ile Ile Gln Glu Phe Pro Ala Leu Gln Glu Arg Asn Tyr Ser Ile Tyr
327 1185 1190 1195
329 ttg aac cat acc atg tta ttg aaa gca ata ctc tta cac tgt ggg atc 3707

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 10/04/2000

PATENT APPLICATION: US/09/515,806

TIME: 22:32:06

Input Set : A:\38155002.app

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L:1222 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1222 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1222 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
L:1225 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1225 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
M:340 Repeated in SeqNo=5
L:1228 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1228 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1231 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1231 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1234 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1234 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1237 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1237 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1240 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1240 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1243 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1243 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1246 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1246 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1249 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1249 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1252 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1252 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1255 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1255 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1258 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1258 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1261 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1261 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1264 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1264 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1267 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1267 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1270 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:1270 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:1291 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:1291 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:1291 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:1294 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:1294 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
M:340 Repeated in SeqNo=6



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1	C.AD	1

Total number of pages: 1

Remarks:

Order of re-scan issued on